

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591,725
Source: IFWP
Date Processed by STIC: 09/13/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,725

DATE: 09/13/2006

TIME: 11:08:53

Input Set : A:\021080002U4.txt

Output Set: N:\CRF4\09132006\J591725.raw

4 <110> APPLICANT: Leonard, Joan
 6 <120> TITLE OF INVENTION: CHICKEN ANEMIA VIRUS VACCINE FROM CELL
 7 LINE
 9 <130> FILE REFERENCE: 02108.0002U4
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/591,725
 12 <141> CURRENT FILING DATE: 2006-09-05
 14 <150> PRIOR APPLICATION NUMBER: PCT/US05/07148
 15 <151> PRIOR FILING DATE: 2005-03-07
 17 <150> PRIOR APPLICATION NUMBER: 60/550,573
 18 <151> PRIOR FILING DATE: 2004-03-05
 20 <160> NUMBER OF SEQ ID NOS: 2
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2294
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Chicken anemia virus
 29 <400> SEQUENCE: 1

30	gcattccgag	tggtaactat	tccatcacca	ttcttagcctg	tacacagaaa	gtcaagatgg	60
31	acgaatcgct	cgacttcgct	cgcgattcgt	cgaaggcggg	gggcccggagg	ccccccgggtg	120
32	ccccccctcc	aacgagtgg	gcatgtacag	gggggtacgt	catcagtaca	gggggggtacg	180
33	tcacaaaaag	gcgttcccgt	acaggggggt	acgtcacgcg	tacagggggg	tacgtcacag	240
34	ccaatcagaa	gctgccacgt	tgcgaaagtg	acgtttcga	aatggggcggc	gcaagcctct	300
35	ctatataattg	agcgcacata	ccggtcggca	gtaggtatac	gcaaggcggt	ccgggtggat	360
36	gcacgggaac	gacggacaac	cggccgctgg	gggcagtgaa	tcggcgccta	gcccggagaggg	420
37	gcagcctggg	cccagcggag	ccgcgcaggg	gcaagtaatt	tcaaatgaac	gctctccaag	480
38	aagatactcc	acccggacca	tcaacgggt	tcagggcacc	aacaagttca	cgccgggttgg	540
39	aaacccctca	ctgcagagag	atccggattt	gtatcgctgg	aattacaatc	actctatcgc	600
40	tgtgtggctg	cgcgaatgct	cgcgctccca	cgctaagatc	tgcaactgcg	gacaattcag	660
41	aaagcaactgg	tttcaagaat	gtgccggact	tgaggaccga	tcaacccaag	cctccctcga	720
42	agaagcgatc	ctgcgacccc	tccgagtaca	gggtaagcga	gctaaaagaa	agcttgatta	780
43	ccactactcc	cagccgaccc	cgaacccgaa	gaagggttat	aagactgtaa	gatggcaaga	840
44	cgagctcgca	gaccgagagg	ccgattttac	gccttcagaa	gaggacgggt	gcaccacctc	900
45	aagcgacttc	gacgaagata	taaatttca	catcgagga	gacagcggta	tcgttagacga	960
46	gcttttagga	aggccttca	caaccccccgc	cccggtacgt	atagtgttag	gctgccgaac	1020
47	ccccaatcta	ccatgactat	ccgcttccaa	ggagtcatct	ttctcacaga	aggactcatt	1080
48	ctgcctaaaa	acagcacagc	ggggggctat	gcagaccaca	tgtacggggc	gagagtgcgc	1140
49	aagatctctg	tgaacctgaa	agagttctgt	ctagcgtcaa	tgaacctgac	atacgtgagc	1200
50	aaaatcgag	gccccatcgc	cggtgagttt	attgcggacg	ggtctaaatc	acaagccqcg	1260
51	gagaactggc	ctaattgctg	gctgccgcta	gataataacg	tgccctccgc	gacaccatcg	1320
52	gcatggtgga	gatgggcctt	aatgatgtat	cagcccacgg	actcttgcgg	gttctttaat	1380
53	caccctaagc	agatgaccct	gcaagacatg	ggtcgcatgt	ttgggggctg	gcaccatttc	1440
54	cgacacattg	aaacccgctt	tcagctcctt	gccactaaga	atgagggatc	cttcagcccc	1500
55	gtggcgagtc	ttctctccca	gggagagttac	ctcacgcgtc	gggacgtatgt	taaatacagc	1560

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56	agcgatcacc	agaaccggtg	gcgaaaaggc	gaacaaccga	tgacgggggg	tattgcttat	1620									
57	gcgaccggga	aatgagacc	cgacgagcaa	cagtaccctg	ctatgcccc	agacccccc	1680									
58	atcatcacca	gtactacagc	gcaaggcacg	caagtccgct	gcatgaatag	cacgcaagct	1740									
59	tgggtgtcat	gggacacata	tatgagctt	gcaacactca	cagcactcgg	tgcacaatgg	1800									
60	tctttcctc	cagggcaacg	ttcagttct	agacggtctt	tcaaccacca	caaggcgaga	1860									
61	ggagccgggg	accccaaagg	ccagagatgg	cacaccctgg	tgccgctcgg	cacggagacc	1920									
62	atcaccgaca	gctacatggg	agcacccgc	tcagagctgg	acacaaattt	ctttacgctt	1980									
63	tacgtacgca	aaggtacaaa	taagtgcag	cagtacaagt	tccgcacagc	tacatacg	2040									
64	ctaaaggagc	cggtaatgaa	gagcattca	tgggcagtgg	tacgcgtcca	gtcggctcgg	2100									
65	caactgggt	acaggcagag	accataacca	tgggacgtca	actgggccaa	cagcaccatg	2160									
66	tactggggcg	ggcagccctg	aaaagggggg	gggctaaagc	ccccccctt	accccccct	2220									
67	gggggggatt	ccccccca	ccccccctt	aatagcact	caataaacgc	agcaattggc	2280									
68	tttatcgac	aatc					2294									
70	<210> SEQ ID NO: 2															
71	<211> LENGTH: 786															
72	<212> TYPE: PRT															
73	<213> ORGANISM: Chicken anemia virus															
75	<400> SEQUENCE: 2															
76	Met	Ala	Arg	Arg	Ala	Arg	Phe									
77	1	5			10		15									
78	Arg	Gly	Arg	Trp	His	His	Leu	Lys	Arg	Leu	Arg	Arg	Tyr	Lys	Phe	
79					20			25				30				
80	Arg	His	Arg	Arg	Gln	Arg	Tyr	Arg	Arg	Arg	Ala	Phe	Arg	Lys	Ala	
81					35			40				45				
82	Phe	His	Asn	Pro	Arg	Pro	Gly	Thr	Tyr	Ser	Val	Arg	Leu	Pro	Asn	Pro
83					50			55				60				
84	Gln	Ser	Thr	Met	Thr	Ile	Arg	Phe	Gln	Gly	Val	Ile	Phe	Leu	Thr	Glu
85	65					70			75				80			
86	Gly	Leu	Ile	Leu	Pro	Lys	Asn	Ser	Thr	Ala	Gly	Gly	Tyr	Ala	Asp	His
87						85			90				95			
88	Met	Tyr	Gly	Ala	Arg	Val	Ala	Lys	Ile	Ser	Val	Asn	Leu	Lys	Glu	Phe
89						100			105				110			
90	Leu	Leu	Ala	Ser	Met	Asn	Leu	Thr	Tyr	Val	Ser	Lys	Ile	Gly	Gly	Pro
91						115			120				125			
92	Ile	Ala	Gly	Glu	Leu	Ile	Ala	Asp	Gly	Ser	Lys	Ser	Gln	Ala	Ala	Glu
93						130			135				140			
94	Asn	Trp	Pro	Asn	Cys	Trp	Leu	Pro	Leu	Asp	Asn	Asn	Val	Pro	Ser	Ala
95	145					150				155				160		
96	Thr	Pro	Ser	Ala	Trp	Trp	Arg	Trp	Ala	Leu	Met	Met	Met	Gln	Pro	Thr
97						165			170				175			
98	Asp	Ser	Cys	Arg	Phe	Phe	Asn	His	Pro	Lys	Gln	Met	Thr	Leu	Gln	Asp
99						180			185				190			
100	Met	Gly	Arg	Met	Phe	Gly	Trp	His	Leu	Phe	Arg	His	Ile	Glu	Thr	
101						195			200				205			
102	Arg	Phe	Gln	Leu	Leu	Ala	Thr	Lys	Asn	Glu	Gly	Ser	Phe	Ser	Pro	Val
103						210			215				220			
104	Ala	Ser	Leu	Leu	Ser	Gln	Gly	Glu	Tyr	Leu	Thr	Arg	Arg	Asp	Asp	Val
105	225					225			230				235			240
106	Lys	Tyr	Ser	Ser	Asp	His	Gln	Asn	Arg	Trp	Arg	Lys	Gly	Glu	Gln	Pro

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107	245	250	255	
108	Met Thr Gly Gly Ile Ala Tyr Ala Thr Gly Lys Met Arg Pro Asp Glu			
109	260	265	270	
110	Gln Gln Tyr Pro Ala Met Pro Pro Asp Pro Pro Ile Ile Thr Ser Thr			
111	275	280	285	
112	Thr Ala Gln Gly Thr Gln Val Arg Cys Met Asn Ser Thr Gln Ala Trp			
113	290	295	300	
114	Trp Ser Trp Asp Thr Tyr Met Ser Phe Ala Thr Leu Thr Ala Leu Gly			
115	305	310	315	320
116	Ala Gln Trp Ser Phe Pro Pro Gly Gln Arg Ser Val Ser Arg Arg Ser			
117	325	330	335	
118	Phe Asn His His Lys Ala Arg Gly Ala Gly Asp Pro Lys Gly Gln Arg			
119	340	345	350	
120	Trp His Thr Leu Val Pro Leu Gly Thr Glu Thr Ile Thr Asp Ser Tyr			
121	355	360	365	
122	Met Gly Ala Pro Ala Ser Glu Leu Asp Thr Asn Phe Phe Thr Leu Tyr			
123	370	375	380	
124	Val Ala Gln Gly Thr Asn Lys Ser Gln Gln Tyr Lys Phe Gly Thr Ala			
125	385	390	395	400
126	Thr Tyr Ala Leu Lys Glu Pro Val Met Lys Ser Asp Ser Trp Ala Val			
127	405	410	415	
128	Val Arg Val Gln Ser Val Trp Gln Leu Gly Asn Arg Gln Arg Pro Tyr			
129	420	425	430	
130	Pro Trp Asp Val Asn Trp Ala Asn Ser Thr Met Tyr Trp Gly Gly Gln			
131	435	440	445	
132	Pro Met His Gly Asn Asp Gly Gln Pro Ala Ala Gly Gly Ser Glu Ser			
133	450	455	460	
134	Ala Leu Ser Arg Glu Gly Gln Pro Gly Pro Ser Gly Ala Ala Gln Gly			
135	465	470	475	480
136	Gln Val Ile Ser Asn Glu Arg Ser Pro Arg Arg Tyr Ser Thr Arg Thr			
137	485	490	495	
138	Ile Asn Gly Val Gln Ala Thr Asn Lys Phe Thr Ala Val Gly Asn Pro			
139	500	505	510	
140	Ser Leu Gln Arg Asp Pro Asp Trp Tyr Arg Trp Asn Tyr Asn His Ser			
141	515	520	525	
142	Ile Ala Val Trp Leu Arg Glu Cys Ser Arg Ser His Ala Lys Ile Cys			
143	530	535	540	
144	Asn Cys Gly Gln Phe Arg Lys His Trp Phe Gln Glu Cys Ala Gly Leu			
145	545	550	555	560
146	Glu Asp Arg Ser Thr Gln Ala Ser Leu Glu Glu Ala Ile Leu Arg Pro			
147	565	570	575	
148	Leu Arg Val Gln Gly Lys Arg Ala Lys Arg Lys Leu Asp Tyr His Tyr			
149	580	585	590	
150	Ser Gln Pro Thr Pro Asn Arg Lys Lys Val Tyr Lys Thr Val Arg Trp			
151	595	600	605	
152	Gln Asp Glu Leu Ala Asp Arg Glu Ala Asp Phe Thr Pro Ser Glu Glu			
153	610	615	620	
154	Asp Gly Gly Thr Thr Ser Ser Asp Phe Asp Glu Asp Ile Asn Phe Asp			
155	625	630	635	640

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156 Ile Gly Gly Asp Ser Gly Ile Val Asp Glu Leu Leu Gly Arg Pro Phe
157 645 650 655
158 Thr Thr Pro Ala Pro Val Arg Ile Val Met Asn Ala Leu Gln Glu Asp
159 660 665 670
160 Thr Pro Pro Gly Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg
161 675 680 685
162 Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly
163 690 695 700
164 Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro
165 705 710 715 720
166 Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Ser Thr Gly Phe Lys
167 725 730 735
168 Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys
169 740 745 750
170 Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser
171 755 760 765
172 Leu Ile Thr Thr Pro Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile
173 770 775 780
174 Arg Leu
175 785

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number